

IN THE SPECIFICATION

Please replace the paragraph on page 20, lines 15-29, with the following paragraph.:

Fig. 4. Comparison of the predicted amino acid sequence of the erbB-3 polypeptide with other receptor-like tyrosine kinases. The amino acid sequence is shown in single letter code (SEQ ID NO: 4) and is numbered on the right. The putative extracellular domain (light shading) extends between the predicted signal sequence (solid box) at the amino-terminus and a single hydrophobic 20 transmembrane region (solid box) within the polypeptide. The two cysteine clusters (Cys) in the extracellular domain and the predicted tyrosine kinase domain (TK) within the cytoplasmic portion of the polypeptide are outlined by dark shading. The putative ATP-binding site at the amino-terminus of the TK domain is circled. Potential autophosphorylation sites within the carboxyl- 25 terminal domain (COOH) are indicated by asterisks. Potential N-linked glycosylation sites ('-') are marked above the amino acid sequence. The percentage of amino acid homology of erbB-3 in individual domains with erbB-2, EGFR, met, eph, insulin receptor (IR), and fi is listed below. Less than 16% identity is denoted by (-);